

BASE COUNT	7 a	9 c	4 g	8 t	1 others
ORIGIN					
Query Match		0.7%;	Score 28;	DB 6;	Length 29;
Best Local Similarity		96.6%;	Pred. No. 2.9e+04;		
Matches	28;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
OY	75	aaggaatcagctgtgtgagctcagcag	103		
Db	29	AAGGAATTCAGTGTGTGAGTCTCAGCNG	1		
RESULT 2					
LOCUS	ROTVP7AK		87 bp ss-RNA	linear	VRL 23-SEP-1994
DEFINITION	Homo sapiens rotavirus 2 (strain 2743)		outer capsid protein (VP7)		
ACCSSION	M37350				
VERSION	M37350.1		GI:548268		
KEYWORDS	VP7 gene; outer capsid protein.				
SOURCE	Human rotavirus 2 (strain 2743)		RNA.		
ORGANISM	Human rotavirus 2				
REFERENCE	1 (bases 1 to 87)				
AUTHORS	Green,K.Y., Sears,J.F., Taniguchi,K., Midtun,K., Hoshino,Y., Gorzjilib,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J.				
TITLE	Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene				
JOURNAL	J. Virol.		62, 1819-1823	(1988)	
MEDLINE	88188272				
FEATURES					
source	Location/Qualifiers				
	1..87				
	/organism="Human rotavirus 2"				
	/strain="2743"				
	/db_xref="taxon:36429"				
gene	1..87				
	/gene="VP7"				
	<1..>87				
CDS	/gene="VP7"				
	/codon_start=1				
	/product="outer capsid protein"				
	/protein_id="AA047369.1"				
	/db_xref="GI:548269"				
	/translation="AAKNEISDDEMENTKTITDVSTFEIVASS"				
BASE COUNT	32 a	11 c	22 g	22 t	
ORIGIN					
Query Match		0.7%;	Score 27.2;	DB 14;	Length 87;
Best Local Similarity		61.1%;	Pred. No. 5.2e+04;		
Matches	44;	Conservative	0;	Mismatches	28; Indels 0; Gaps 0;
OY	818	ctcgtgaagtgatattcagctgagatgagatgagacactatagctcgtctaattgagtgaca	877		
Db	8	CTAATAAAGAGATTTCAGATGATGAGTAATGAGAAATACTAATAACTACGAGACGTGAGTACAT	67		
OY	878	ctgaggtttatg 889			
Db	68	TTTGAGATAGTTG 79			
RESULT 3					
LOCUS	ROTVP7AL		87 bp ss-RNA	linear	VRL 23-SEP-1994
DEFINITION	Homo sapiens rotavirus 2 (strain 2899)		outer capsid protein (VP7)		
ACCSSION	M37351				
VERSION	M37351.1		GI:548270		
KEYWORDS	VP7 gene; outer capsid protein.				
SOURCE	Human rotavirus 2 (strain 2899)		RNA.		
ORGANISM	Human rotavirus 2				

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REFERENCE      Viruses; dsRNA viruses; Reoviridae; Rotavirus.
AUTHORS       1 (bases 1 to 87)
              Green,K.Y., Sears,J.F., Taniguchi,K., Midhun,K., Hoshino,Y.,
              Gorzjila,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M.
              and Flores,J.
TITLE         Prediction of human rotavirus serotype by nucleotide sequence
              analysis of the VP7 protein gene
JOURNAL       J. Virol. 62, 1819-1823 (1988)
MEDLINE       88188272
FEATURES
source        Location/Qualifiers
              1..87
               /organism="Human rotavirus 2"
               /strain="2899"
               /db_xref="taxon:36429"
gene          1..87
               /gene="VP7"
               <1..>87
CDS           /gene="VP7"
               /codon_start=1
               /product="Outer capsid protein"
               /protein_id="AA47370.1"
               /db_xref="GI:548271"
               /translation="AEAKNEISDEMENTKTIDVSTREIVASS"
BASE COUNT   32 a 11 c 22 g 22 t
ORIGIN
Query Match    0.7%; Score 27.2; DB 14; Length 87;
Best Local Similarity 61.1%; Pred. No. 5,2e+04;
Matches 44; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
OY            818 ctgtaagtgattcagtgcataatgaatgaacactatagctgctaattgagtaca 877
Db            8 CTAAAAAGACATCTTCACATGATCATGAATGGCAAAAATACTAATAACTACGCAGCGATACAT 67
OY            878 ctgaatttcatg 889
Db            68 TTGAGATAGTTC 79
RESULT 4
AF213231      89 bp DNA linear MAM 09-FEB-2001
LOCUS         AF213231
DEFINITION   Bison bison clone 15.1.1 microsatellite BMS410-89.
VERSION       AF213231
KEYWORDS     AF213231.1 GI:11837834
SOURCE       American bison.
ORGANISM     Bison bison
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bison.
REFERENCE    1 (bases 1 to 89)
AUTHORS     Schnabel,R.D., Ward,T.J. and Derr,J.N.
TITLE       Validation of 15 microsatellites for percentage testing in North
             American bison, Bison bison and domestic cattle
JOURNAL     Anim. Genet. 31 (6), 360-366 (2000)
MEDLINE     21070477
REFERENCE    2 (bases 1 to 89)
AUTHORS     Schnabel,R.D., Ward,T.J. and Derr,J.N.
TITLE       Direct Submission
JOURNAL     Submitted (07-DEC-1999) Veterinary Pathobiology, Texas A&M
             University, Bldg. 1197 Rm.226, College Station, TX 77843-4467, USA
FEATURES
source        Location/Qualifiers
              1..89
               /organism="Bison bison"
               /db_xref="taxon:9901"
               /clone="15.1.1"
primer_bind   1..22
repeat_region 1..89
              /note="microsatellite BMS410-89"
              /rfc_type=tandem
primer_bind   70..89

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BASE COUNT	29 a	33 c	8 g	19 t
ORIGIN				
Query Match		0.6%;	Score 25.8;	DB 4; Length 89;
Best Local Similarity		56.5%;	Pred. No. 1.3e+05;	
Matches 48;	Conservative	0;	Mismatches 37;	Indels 0; Gaps 0;
OY 1450	ttctgaatgtgctgctgctgacccaccgaatcctcaacacctgcaaacacactctaccag	1509		
DB 1	TTGGCCACACATTTACCTCTTTCATAGACGCACACACACACACACACACACACACAC	60		
OY 1510	gtcaatgcaaacagcgctgctttac	1534		
DB 61	GTGGTTATTAACACCCACAGCTTTTC	85		
RESULT 5				
LOCUS	ROTVP7AJ	87 bp ss-RNA	linear	VRL 23-SEP-1994
DEFINITION	Homo sapiens rotavirus 2 (strain HNI26) outer capsid protein (VP7)			
ACCESSION	M37349			
VERSION	M37349.1	GI:548266		
KEYWORDS	VP7 gene; outer capsid protein.			
SOURCE	Human rotavirus 2 (strain HNI26) RNA.			
ORGANISM	Human rotavirus 2			
REFERENCE	1 (bases 1 to 87)			
AUTHORS	Green,K.Y., Sears,J.F., Taniguchi,K., Midhun,K., Hoshino,Y., Gorziglia,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J.			
TITLE	Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene			
JOURNAL	J. Virol. 62, 1819-1823 (1988)			
MEDLINE	88188272			
FEATURES				
source	Location/Qualifiers			
	1..87			
	/organism="Human rotavirus 2"			
	/strain="HNI26"			
	/db_xref="taxon:36429"			
	1..87			
	/gene="VP7"			
	<1..>87			
	/gene="VP7"			
	/codon_start=1			
	/product="outer capsid protein"			
	/protein_id="AA047368.1"			
	/db_xref="GI:548267"			
	/translation="TEAKNEISDDEMENTKTVDNTEPIVASS"			
BASE COUNT	34 a	11 c	19 g	23 t
ORIGIN				
Query Match		0.6%;	Score 25.6;	DB 14; Length 87;
Best Local Similarity		59.7%;	Pred. No. 1.4e+05;	
Matches 43;	Conservative	0;	Mismatches 29;	Indels 0; Gaps 0;
OY 818	ctgtgaagtgatcattcagatgagatgaatgaatgacatgacatgctgctaattgagtga	877		
DB 8	CTTAAATAAGAGATTTCATGATGATGATGGAATAACTTAATACTAGGATTAACACAT	67		
OY 878	ctgagtttattcg	889		
DB 68	TTGAGATTTGTTG	79		
RESULT 6				
LOCUS	ROTVP7AM	87 bp ss-RNA	linear	VRL 23-SEP-1994
DEFINITION	Homo sapiens rotavirus 2 (strain C) outer capsid protein (VP7) RNA.			
ACCESSION	M37352			

VERSION	M37352.1	GI:548272
KEYWORDS	VP7 gene; outer capsid protein.	
SOURCE	Human rotavirus 2 (strain C) RNA.	
ORGANISM	Human rotavirus 2	
REFERENCE	Viruses; dsRNA viruses; Reoviridae; Rotavirus.	
AUTHORS	1 (bases 1 to 87) Green,K.Y., Sears,J.F., Taniguchi,K., Midtun,K., Hoshino,Y., Gorziglia,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J.	
TITLE	Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene	
JOURNAL	J. Virol. 62, 1819-1823 (1988)	
MEDLINE	88188272	
FEATURES	Location/Qualifiers	
source	1..87	
	/organism="Human rotavirus 2"	
	/strain="C"	
	/db_xref="taxon:36429"	
gene	1..87	
	/gene="vp7"	
CDS	<1..>87	
	/gene="VP7"	
	/codon_start=1	
	/product="outer capsid protein"	
	/protein_id="AA047371.1"	
	/db_xref="GI:548273"	
	/translation="AEAKNETSDDEMENTKTVDVNTFEIVASS"	
BASE COUNT	33 a	20 g
ORIGIN	11 c	23 t
Query Match	0.6%	Score 25.6; DB 14; Length 87;
Best Local Similarity	59.7%;	Pred. No. 1.4e+05;
Matches 43; Conservative 0;	Mismatches 29;	Indels 0; Gaps 0;
OY	818 ctctgaagtgatcattcatgatgataagaacacactatgcctcattgagtgcaca	877
Db	8 CTAAATAAGAGATTTCACAGTGTGATGATGGAAAATCTAATAACTACGGATGAACACAT	67
OY	878 ctgaagtttaatg 889	
Db	68 TTGAGATTGTTG 79	
RESULT	7	
ROTVP7AN	ROTVP7AN	87 bp ss-RNA linear VRL_23-SEP-1994
LOCUS	Homo sapiens rotavirus 2 (strain V197) outer capsid protein (VP7)	
DEFINITION	RNA, partial cds.	
ACCESSION	M37353	
VERSION	M37353.1	GI:548274
KEYWORDS	VP7 gene; outer capsid protein.	
SOURCE	Human rotavirus 2 (strain V197) RNA.	
ORGANISM	Human rotavirus 2	
REFERENCE	Viruses; dsRNA viruses; Reoviridae; Rotavirus.	
AUTHORS	1 (bases 1 to 87) Green,K.Y., Sears,J.F., Taniguchi,K., Midtun,K., Hoshino,Y., Gorziglia,M., Nishikawa,K., Urasawa,S., Kapikian,A.Z., Chanock,R.M. and Flores,J.	
TITLE	Prediction of human rotavirus serotype by nucleotide sequence analysis of the VP7 protein gene	
JOURNAL	J. Virol. 62, 1819-1823 (1988)	
MEDLINE	88188272	
FEATURES	Location/Qualifiers	
source	1..87	
	/organism="Human rotavirus 2"	
	/strain="V197"	
	/db_xref="taxon:36429"	
gene	1..87	
	/gene="VP7"	
CDS	<1..>87	
	/gene="VP7"	
	/codon_start=1	

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/product="outer capsid protein"
/protein_id="AAA4/372.1"
/db_xref="GI:548275"
/translation="AAEKNEISDDEMENTKTTDVNTPEIVASS"

BASE COUNT      33 a      11 c      20 g      23 t
ORIGIN

Query Match      0.6%; Score 25.6; DB 14; Length 87;
Best Local Similarity 59.7%; Pred. No. 1.4e+05;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 818 ctgtgaagtgatttcagtgatgaatgaatgaacactaagctgaattgaatgaacaa 877
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 CTAAAGAAAGAGATTCAGATGATGAATGGGAAATTAATACTAGCATGTAAACACAT 67

QY 878 ctgaattctatg 889
    ||| ||| |||
Db 68 TTGAGATTGTTC 79

RESULT 8
AF213232      93 bp      DNA      linear      MM 09-FEB-2001
LOCUS      AF213232
DEFINITION      Bison bison clone 13.13.1 microsatellite BMS410-93.
ACCESSION      AF213232
VERSION      AF213232.1 GI:11837835
KEYWORDS
SOURCE      American bison.
ORGANISM      Bison bison.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bison.
REFERENCE      1 (bases 1 to 93)
AUTHORS      Schnabel,R.D., Ward,T.J. and Derr,J.N.
TITLE      Validation of 15 microsatellites for parentage testing in North
JOURNAL      American bison, Bison bison and domestic cattle
MEDLINE      Anim. Genet. 31 (6), 360-366 (2000)
21070477
REFERENCE      2 (bases 1 to 93)
AUTHORS      Schnabel,R.D., Ward,T.J. and Derr,J.N.
TITLE      Direct Submission
JOURNAL      Submitted (07-DEC-1999) Veterinary Pathobiology, Texas A&M
University, Bldg. 1197 Rm.226, College Station, TX 77843-4467, USA
FEATURES
source
    1..93
    /organism="Bison bison"
    /db_xref="taxon:9901"
    /clone="13.13.1"
    primer_bind
        1..22
    repeat_region
        1..93
    /note="microsatellite BMS410-93"
    /rpt_type=tandem

BASE COUNT      31 a      35 c      8 g      19 t
ORIGIN

Query Match      0.6%; Score 25.4; DB 4; Length 93;
Best Local Similarity 58.7%; Pred. No. 1.6e+05;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1460 tgcgtgctgagccaccagaaatccctacacccgcgaacacactctacagtcattgcaa 1519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 TTCTTTTATAGACGACACACACACACACACACACACACACACACACACACACACACAC 74

QY 1520 acagagcctgcttacc 1534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 ACACCACAGCTTTTC 89

RESULT 9
AF272967/c

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LOCUS      AF272967      94 bp      DNA      linear      VRT 08-JAN-2002
DEFINITION      Mastacembelus aculeatus doublesex-like protein Dmrt2a gene, partial
ACCESSION      AF272967
VERSION      AF272967.1 GI:10567711
KEYWORDS
SOURCE      Mastacembelus aculeatus.
ORGANISM      Mastacembelus aculeatus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Sybranchiiformes;
Mastacembelidae; Mastacembelus.
REFERENCE      1 (bases 1 to 94)
AUTHORS      Huang,X. and Zhou,R.
TITLE      A conserved family of doublesex related genes from fish
JOURNAL      J. Exp. Zool. (2002) In press
2 (bases 1 to 94)
REFERENCE      Huang,X. and Zhou,R.
AUTHORS      Direct Submission
TITLE      Submitted (30-MAY-2000) Genetics, Wuhan University, LuoJia, Wuhan,
Hubel 430072, P.R. China
FEATURES
source
    1..94
    /organism="Mastacembelus aculeatus"
    /db_xref="taxon:138129"
    mRNA
    <1..>94
    /product="doublesex-like protein Dmrt2a"
    <1..>94
    /note="contains DM domain"
    /codon_start=2
    /product="doublesex-like protein Dmrt2a"
    /protein_id="MAG18552.1"
    /db_xref="GI:10567712"
    /translation="VWSCIKGRKRCFRMRNDQCQNCALLVVERQRV"

BASE COUNT      13 a      23 c      39 g      19 t
ORIGIN

Query Match      0.6%; Score 25.4; DB 5; Length 94;
Best Local Similarity 61.2%; Pred. No. 1.6e+05;
Matches 41; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 166 cccctgattctctctctgcccagatgattgactggaagtacctctgattccaaa 225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 CCGCTGCTCTCCACACAGCAGCAGCAGTTCGCGACTGCGACGCTCCAGCGGACGAA 32

QY 226 cttctg 232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31 GCGCTTG 25

RESULT 10
I71468
LOCUS      I71468      70 bp      DNA      linear      PAT 03-APR-1998
DEFINITION      Sequence 9 from patent US 5681942.
ACCESSION      I71468
VERSION      I71468.1 GI:3007603
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 70)
AUTHORS      Buchwald,M., Strathdee,C.A., Wevrick,R. and Mathew,C.George.Porter.
TITLE      Fanconi Anemia Type C gene
JOURNAL      Patent: US 5681942-A 9/28-OCT-1997;
FEATURES
source
    1..70
    /organism="unknown"

BASE COUNT      26 a      8 c      11 g      25 t
ORIGIN

Query Match      0.6%; Score 25; DB 6; Length 70;

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Best Local Similarity 61.5%: Pred. No. 2e+05;	
Matches 40:	Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 3449	aaatgttaaatggtctctgcgaacctcttgggttaagaggtcaatgcgaagacagcat 3508
Db 4	AGAGAGTAAATCTTGCTGCACCTCTTTGATTAATTAATTATTTAAAGTGTGCTT 63
Qy 3509	accaa 3513
Db 64	AAAAA 68
RESULT 11	
AF174509/c	97 bp DNA linear VRT 20-APR-2000
LOCUS	AF174509
DEFINITION	Torrenthophryne aspinia K12-93A011 cytochrome b gene, partial cds;
ACCESSION	AF174509
VERSION	AF174509.1 GI:7620455
KEYWORDS	
ORGANISM	Torrenthophryne aspinia.
SOURCE	Mitochondrion Torrenthophryne aspinia
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufonidae;
TITLE	Torrenthophryne.
JOURNAL	1 (bases 1 to 97)
MEDLINE	Li,J.W., Lathrop,A., Fu,J., Yang,D. and Murphy,R.W.
PUBMED	Phylogeny of East Asian bufonids inferred from mitochondrial DNA
REFERENCE	sequences (Anura: Amphibia)
JOURNAL	Mol. Phylogenet. Evol. 14 (3), 423-435 (2000)
FEATURES	2 (bases 1 to 97)
source	Li,J.W., Lathrop,A., Fu,J. and Murphy,R.W.
	Direct Submission
	Submitted (26-JUL-1999) CCB, Royal Ontario Museum, 100 Queen's
	Park, Toronto, Ontario M5S 2C6, Canada
	Location/Qualifiers
	1..97
	/organism="Torrenthophryne aspinia"
	/organelle="mitochondrion"
	/specimen_voucher="K12-93A011"
	/db_xref="taxon:103606"
	/country="China: Yunnan, Yangbi Co."
	<1..>97
	/product="cytochrome b"
	<1..97
	/codon_start=2
	/transl_table=2
	/product="cytochrome b"
	/protein_id="AA64628.1"
	/db_xref="GI:7620456"
	/translation="MIGOLASVSSEFLFIITFTPLGLTENKTLQD"
BASE COUNT	28 a 31 c 8 g 30 t
ORIGIN	
Query Match	0.6%: Score 24.8; DB 5; Length 97;
Best Local Similarity 54.3%: Pred. No. 2.4e+05;	
Matches 50:	Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy 3908	agttcaatgaagatggtctcttalttgacaatacagtgtaagaagaagaagccgg 3967
Db 93	AGTTGAGTTAGTTTGCTTTGCGTGAGTCCGAGAAAGGGGCTAAATAATGATTAAGATTAA 34
Qy 3968	ctgaaggaacgaagcctcagaagccacttct 3999
Db 33	AAGTAGGAGACGGAAGCTAATTGGCCATTAT 2
RESULT 12	
AF174510/c	97 bp DNA linear VRT 20-APR-2000
LOCUS	AF174510

DEFINITION	Torrrentophryne tuberospina K12-91A089 cytochrome b gene, partial cds: mitochondrial gene for mitochondrial product.		
ACCESSION	AF174510		
VERSION	AF174510.1 GI:7620457		
KEYWORDS	Torrrentophryne tuberospina.		
SOURCE	Torrrentophryne tuberospina.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufonidae; Torrrentophryne.		
REFERENCE	1 (bases 1 to 97)		
AUTHORS	Liu,W., Lathrop,A., Fu,J., Yang,D. and Murphy,R.W.		
TITLE	Phylogeny of East Asian bufonids inferred from mitochondrial DNA sequences (Anura: Amphibia)		
JOURNAL	Mol. Phylogenet. Evol. 14 (3), 423-435 (2000)		
MEDLINE	20179527		
PUBMED	10712847		
REFERENCE	2 (bases 1 to 97)		
AUTHORS	Liu,W., Lathrop,A., Fu,J. and Murphy,R.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-JUL-1999) CIBC, Royal Ontario Museum, 100 Queen's Park, Toronto, Ontario M5S 2C6, Canada		
FEATURES	location/Qualifiers		
SOURCE	1..97		
	/organism="Torrrentophryne tuberospina"		
	/organelle="mitochondrion"		
	/specimen_voucher="K12-91A089"		
	/db_xref="taxon:103607"		
	/country="China: Yunnan, Tengchong Co."		
	<1..>97		
	/product="cytochrome b"		
	<1..97		
	/transl_table=2		
	/codon_start=2		
	/product="cytochrome b"		
	/protein_id="AAFG4629.1"		
	/db_xref="GI:7620458		
	/translation="MIGQLASVSYFLFIIFTPPLGLTENKLTQL"		
BASE COUNT	29 a	30 c	8 g
ORIGIN	30 t		
Query Match	0.6%;	Score 24.8;	DB 5; Length 97;
Best Local Similarity	54.3%;	Pred. No. 2.4e+05;	
Matches	50;	Conservative	0; Mismatches 42; Indels 0; Gaps 0;
QY	3908	agttaaatgagatgctcccttattgtgaacataacagcggcgaagaagaagacgcgg	3967
DB	93	AGTTAAGTTAGTTTCTTCTGTGATCGCGAAGAGGGGGTGAAATGATAAAGATTAAAG	34
QY	3968	ctgaagaacacgaacgccacagagacacttct	3999
DB	33	AAGTAGGAGACGACGAAGCTAATTGACCGATTAA	2
RESULT 13	SYNDEL951		
LOCUS	SYNDEL951/c		
DEFINITION	X.laeviss DNA containing insertion element Tn9, deleted element, 5' end.		
ACCESSION	M10780		
VERSION	M10780.1 GI:208208		
KEYWORDS	deletion; deletion mutant.		
SEGMENT	1 of 2		
SOURCE	X.laeviss oocyte 5S DNA and transposon Tn9 DNA, combined in plasmid pMB9, mutants 95 and 10.		
ORGANISM	X.laeviss		
REFERENCE	1 (bases 1 to 90)		
AUTHORS	Fedoroff,N.V.		
TITLE	Structure of deletion derivatives of a recombinant plasmid containing the transposable element Tn9 in the spacer sequence of Xenopus laevis 5S DNA		

JOURNAL Cold Spring Harb. Symp. Quant. Biol. 43, 1287-1292 (1979)
 MEDLINE 80023367
 FEATURES Location/Qualifiers
 source 1..90
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 BASE COUNT 28 a 9 c 8 g 45 t
 ORIGIN

Query Match 0.6%; Score 24.6; DB 12; Length 90;
 Best Local Similarity 55.2%; Pred. No. 2.7e+05;
 Matches 48; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 3089 ttacacagacacatgaatgaagccctctgttagattgaattcctgcacacagacac 3148
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 90 TTGAAACTTTGAAAAAATTAACCTTTGAAAACTTTGAAAAATCAACTTTGAAAAAGT 31

QY 3149 ggtgaccttaaaaaatttaattca 3175
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 30 TGAATACTTTGAAAAATTAACCTTGA 4

RESULT 14
 AF326227
 LOCUS AF326227 70 bp DNA linear PLN 02-MAR-2001
 DEFINITION Arabidopsis thaliana small nucleolar RNA R83, complete sequence.
 ACCESSION AF326227
 VERSION AF326227.1 GI:13183695
 KEYWORDS thale cress.
 SOURCE Arabidopsis thaliana
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 70)
 Barneche,F., Gaspin,C., Guyot,R. and Echeverria,M.
 Extensive characterization of methylation guide small nucleolar
 RNAs in Arabidopsis thaliana
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 70)
 Barneche,F., Gaspin,C., Guyot,R. and Echeverria,M.
 Direct Submission
 TITLE Submitted (06-DIC-2000) Laboratoire Genome et Developpement des
 JOURNAL Plantes, Universite de Perpignan, UMR CNRS 5096, Avenue de
 Villeneuve, Perpignan, Pyrenees Orientales 66860, France
 FEATURES Location/Qualifiers
 source 1..70
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /dev_stage="seedling"
 /note="ecotype: Columbia 0"
 1..70
 /note="Atsnor83"
 /product="small nucleolar RNA R83"
 /evidence="experimental"
 BASE COUNT 19 a 9 c 19 g 23 t
 ORIGIN

Query Match 0.6%; Score 24.4; DB 8; Length 70;
 Best Local Similarity 63.8%; Pred. No. 2.9e+05;
 Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 3764 aagatgagggacatttgagaatcagtgatgcagaagcacaagccttgaanaa 3821
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 5 ATGATGATGGGATTGTGGAGATTACGATGAGGATGTACAGCTCCCTCTGTGATTAA 62

RESULT 15
 LOCUS S45981 86 bp RNA linear BCT 07-MAY-1993
 DEFINITION Selenoprotein A [Clostridium purinolyticum, Genomic RNA, 86 nt].

ACCESSION S45981
 VERSION S45981.1 GI:1679975
 KEYWORDS
 SOURCE Clostridium purinolyticum.
 ORGANISM Clostridium purinolyticum.
 Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 Clostridium.
 REFERENCE 1 (bases 1 to 86)
 AUTHORS Garcia,G.E. and Stadman,T.C.
 TITLE Selenoprotein A, a component of the glycine reductase complex from
 Clostridium purinolyticum: nucleotide sequence of the gene shows
 that selenocysteine is encoded by UGA
 JOURNAL J. Bacteriol. 173 (15), 4908 (1991)
 MEDLINE 91310603
 REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gtblseq 45981] from the original journal article.
 COMMENT This sequence comes from 5a.
 On Nov 21, 1996 this sequence version replaced gi:1619721.
 *ERRATUM** Vol. 173, no. 6, p. 2097.
 FEATURES Location/Qualifiers
 source 1..86
 /organism="Clostridium purinolyticum"
 /db_xref="taxon:1503"
 1..86
 /gene="Selenoprotein A"
 BASE COUNT 27 a 14 c 24 g 21 t
 ORIGIN

Query Match 0.6%; Score 24.4; DB 1; Length 86;
 Best Local Similarity 56.1%; Pred. No. 3e+05;
 Matches 46; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1130 aatgatagcaaaaatgatgagcagccatccatcattctgttagagttaaag 1189
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3 AATGTTTGTCTGAACCTGCAGCAGGACTATGAGATCTGGAGATCCAAACAAAAGTTAAAG 62

QY 1190 cggctccatctggtacacagc 1211
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 63 ATGCTGCTGAGTCATTCGAGAGC 84

Search completed: August 13, 2002, 22:40:53
 Job time: 11355 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 20:24:26 ; Search time 416.67 Seconds
(without alignments)
17034.402 Million cell updates/sec

Title: US-09-301-380-1
Perfect score: 4134
Sequence: 1 ctctaaagctcccgcatga.....tgggtagagagatatatttc 4134

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 segs, 858457221 residues
Total number of hits satisfying chosen parameters: 1183566

Minimum DB seq length: 15
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq.032802:*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
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17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	2.2	91	22	AAK51341
2	91	2.2	91	22	AA157408
3	50	1.2	51	22	AA126826
4	48.8	1.2	60	21	AA238172
5	38	0.9	38	21	AA238153
6	28.8	0.7	97	21	AA214618
7	28	0.7	29	19	AAV40897
8	28	0.7	29	21	AA64165
9	28	0.7	29	21	AA98540

C	10	26.4	0.6	50	21	AA238180	Human NR-CAM gene
C	11	26	0.6	82	17	AA744495	Murine p57KIP2 gen
C	12	26	0.6	96	22	ABA36168	Probe #14634 for g
C	13	26	0.6	96	22	AA749423	Probe #18109 used
C	14	25.8	0.6	71	13	AA024813	Universal promoter
C	15	25.8	0.6	73	13	AA024815	Universal promoter
C	16	25.4	0.6	88	21	AAA28515	Primer PRIL 5' for
C	17	25.2	0.6	72	22	AA61467	MBP/BMP fusion con
C	18	25	0.6	39	21	AA238169	Antisense NR-CAM 1
C	19	25	0.6	65	13	AA024812	Universal promoter
C	20	25	0.6	67	13	AA024814	Universal promoter
C	21	25	0.6	70	14	AA051433	Human FACC intron
C	22	25	0.6	93	16	AA728332	Human gene signatu
C	23	24.8	0.6	86	16	AA19434	Human gene signatu
C	24	24.8	0.6	93	22	ABA50916	Human breast cell
C	25	24.8	0.6	93	22	ABA68894	Human breast liver
C	26	24.8	0.6	93	22	ABA35845	Probe #14311 for g
C	27	24.8	0.6	93	22	AAK17426	Human brain expres
C	28	24.8	0.6	93	22	AAK43012	Human bone marrow
C	29	24.8	0.6	93	22	AA123781	Probe #13714 for g
C	30	24.8	0.6	93	22	AA149091	Probe #17777 used
C	31	24.8	0.6	93	22	AA109387	Probe #378 used t
C	32	24.6	0.6	50	21	AA252309	Human secreted pro
C	33	24.4	0.6	38	21	AA238156	Human NR-CAM gene
C	34	24.4	0.6	38	21	AA238170	Antisense NR-CAM 2
C	35	24.2	0.6	84	18	AA71750	Fibroblast succin
C	36	24.2	0.6	95	22	AA504616	Gene expression pr
C	37	24	0.6	24	21	AA238159	Human NR-CAM gene
C	38	24	0.6	38	21	AA238157	Human NR-CAM gene
C	39	24	0.6	38	21	AA238171	Antisense NR-CAM 2
C	40	24	0.6	92	21	AA17898	CDNA encoding huma
C	41	24	0.6	92	22	AA128636	Colon tumour relat
C	42	24	0.6	100	24	AA598937	Human prostate can
C	43	23.8	0.6	37	21	AA238168	Antisense NR-CAM 1
C	44	23.8	0.6	48	21	AA238179	Human NR-CAM gene
C	45	23.8	0.6	87	19	AA797234	Trimmed enzyme sig

ALIGNMENTS

RESULT 1
AAK51341/C
AAK51341 standard; DNA; 91 BP.

AAK51341:
(first entry)

Human bone marrow expressed single exon probe SEQ ID NO: 25898.

Human: bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukemia; lymphoma; myeloma; ss.

Human sapiens.

WO200157276-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00668.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 XX
 PS Example 4; SEQ ID NO: 25898; 658bp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention.
 XX
 SQ Sequence 91 BP; 24 A; 23 C; 23 G; 21 T; 0 other;

Query Match 2.2%; Score 91; DB 22; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 atgcgcgaaaaagagcgtctatctgcgagagtgccctgattctctctgtagcag 189
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 91 ATGCCGAAAAAGAGCGCTTATCTGCGGGCAGAGTGCCCTGATTCTCTCTGTCAG 32
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 190 atgattagtgacactggaagtacctcttgatc 220
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 31 ATGATTAGTGCACTGGAGTACCTCTTGATC 1

RESULT 2
 AAI57408/C
 ID AAI57408 standard; DNA; 91 BP.
 XX
 AC AAI57408;
 XX
 DT 17-OCT-2001 (first entry)
 XX

DE Probe #26094 used to measure gene expression in human placenta sample.

KM Probe; microarray; human; placenta; antenatal diagnosis;
 KM genetic disorder; ss.
 XX

OS Homo sapiens.
 XX

PN WO200157272-A2.
 XX

PD 09-AUG-2001.
 XX

PF 30-JAN-2001; 2001WO-US00663.
 XX

PR 04-FEB-2000; 2000US-0180312.
 XX

PR 26-MAY-2000; 2000US-0207456.
 XX

PR 30-JUN-2000; 2000US-0608408.
 XX

PR 03-AUG-2000; 2000US-0632366.
 XX

PR 21-SEP-2000; 2000US-0234687.
 XX

PR 27-SEP-2000; 2000US-0236359.
 XX

PR 04-OCT-2000; 2000GB-0024263.
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX

WPI; 2001-488897/53.
 XX

PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX
 XX Claim 25; SEQ ID NO 26094; 654bp; English.
 CC The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for

CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders.
 XX

SQ Sequence 91 BP; 24 A; 23 C; 23 G; 21 T; 0 other;

Query Match 2.2%; Score 91; DB 22; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 atgcgcgaaaaagagcgtctatctgcgagagtgccctgattctctctgtagcag 189
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 91 ATGCCGAAAAAGAGCGCTTATCTGCGGGCAGAGTGCCCTGATTCTCTCTGTCAG 32
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 190 atgattagtgacactggaagtacctcttgatc 220
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 31 ATGATTAGTGCACTGGAGTACCTCTTGATC 1

RESULT 3
 AAL26826
 ID AAL26826 standard; DNA; 51 BP.
 XX
 AC AAL26826;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #34.
 XX

KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KM neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KM amyloid protein; angiopoietin; apoptosis related protein; cadherin;
 KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KM complement related protein; cytochrome; kinesin; cytokine; interferon;
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KM multifactorial disease; autoimmune disease; infection;
 KM nervous system disease; ss.
 XX

OS Homo sapiens.
 XX

PN WO200147944-A2.
 XX

PD 05-JUL-2001.
 XX

PF 28-DEC-2000; 2000WO-US35498.
 XX

PR 28-DEC-1999; 99US-0173419.
 XX

PR 27-DEC-2000; 2000US-0173419.
 XX

PA (CURA-) CURAGEN CORP.
 XX

PI Shinkets RA, Leach M;
 XX

WPI; 2001-465210/50.
 XX

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 XX Claim 1; Page 1409; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune

CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX Sequence 51 BP; 14 A; 13 C; 11 G; 12 T; 1 other;

Query Match 1.2%; Score 50; DB 22; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.00014;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1177 gtttaggttaagcggctccatcgtacacagccctcaaatctgtg 1227
|||||
Db 1 gtttaggttaagcggctccatcgtacacagccctcaaatctgtg 51

RESULT 4
AAZ38172
ID AAZ38172 standard; DNA; 60 BP.

XX AAZ38172;

XX 14-FEB-2000 (first entry)

XX Human Nr-CAM gene fragment.

XX Nr-CAM, neuron-glia-related cell adhesion molecule; cell proliferation;
XX tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;
XX degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;
XX systemic lupus erythematosus; demyelinating disease; growth; human; ss.

XX Homo sapiens.

XX WO9955380-A1.

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-US09039.

XX 27-APR-1998; 98US-0083152.

XX 14-DEC-1998; 98US-0112098.

XX (PACI-) PACIFIC NORTHWEST CANCER FOUND.

XX Murphy GP, Boynton AL, Sehgal A;

XX WPI; 2000-023268/02.

XX Use of neuron-glia-related cell adhesion molecule for developing agents
XX for the diagnosis and treatment of e.g. cancers, hyperproliferative
XX disorders, growth deficiencies, degenerative disorders, trauma or
XX wounds

XX Examples; Page 123; 183pp; English.

XX The invention relates to the use of neuron-glia-related cell adhesion
XX molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or
XX preventing disorders involving cell proliferation. An antisense nucleic
XX acid complementary to at least a portion of an RNA transcript of a
XX Nr-CAM gene can be used to inhibit hyperproliferation of a tumor cell,
XX for the treatment of tumorigenesis. Agents which inhibit and promote
XX Nr-CAM function can be used for the treatment of various diseases and
XX disorders (see AAZ38152 for a detailed description). The products can
XX also be used for detection, diagnosis and production of animal models.
XX The present sequence represents a human Nr-CAM gene fragment against
XX which phosphothioate oligonucleotides are designed.

XX Sequence 60 BP; 22 A; 9 C; 16 G; 13 T; 0 other;

Query Match 1.2%; Score 48.8; DB 21; Length 60;

Best Local Similarity 88.3%; Pred. No. 0.00034;
Matches 53; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 99 accgaggttaagcgtcaatcagcttaataatgcccgaataaagcgtatctcggg 158
|||||
Db 1 aggagtttaagatcgtcaatcagcttaataatgcccgaataaagcgtatctcggg 60

RESULT 5
AAZ38153
ID AAZ38153 standard; DNA; 38 BP.

XX AAZ38153;

XX 14-FEB-2000 (first entry)

XX Human Nr-CAM gene fragment (basepairs 4097-4134).

XX Nr-CAM, neuron-glia-related cell adhesion molecule; cell proliferation;
XX tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;
XX degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;
XX systemic lupus erythematosus; demyelinating disease; growth; human; ss.

XX Homo sapiens.

XX WO9955380-A1.

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-US09039.

XX 27-APR-1998; 98US-0083152.

XX 14-DEC-1998; 98US-0112098.

XX (PACI-) PACIFIC NORTHWEST CANCER FOUND.

XX Murphy GP, Boynton AL, Sehgal A;

XX WPI; 2000-023268/02.

XX Use of neuron-glia-related cell adhesion molecule for developing agents
XX for the diagnosis and treatment of e.g. cancers, hyperproliferative
XX disorders, growth deficiencies, degenerative disorders, trauma or
XX wounds

XX Disclosure; Fig 2C; 183pp; English.

XX The invention relates to the use of neuron-glia-related cell adhesion
XX molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or
XX preventing disorders involving cell proliferation. An antisense nucleic
XX acid complementary to at least a portion of an RNA transcript of a
XX Nr-CAM gene can be used to inhibit hyperproliferation of a tumor cell,
XX for the treatment of tumorigenesis. Agents which inhibit Nr-CAM function
XX can be used to treat or prevent malignancies, e.g. brain cancer,
XX leukemia, B cell lymphoma, premalignant conditions, benign tumors,
XX hyperproliferative disorders or benign dysproliferative disorders. Such
XX treatment is especially useful for treating glioblastoma, glioma,
XX meningioma, astrocytoma, medulloblastoma, neuroectodermal cancer and
XX neuroblastoma, especially glioblastoma multiforme. Agents which promote
XX Nr-CAM function may also be used to treat or prevent degenerative
XX disorders, growth deficiencies, hypoproliferative disorders, physical
XX trauma, lesions or wounds. In particular, they can be used for treating
XX e.g. traumatic, ischemic, malignant and degenerative lesions and
XX alcoholic cerebellar degeneration. Also described is the treatment of
XX lesions associated with systemic diseases e.g. diabetes or systemic lupus
XX erythematosus, lesions caused by toxic substances e.g. alcohol, lead or
XX other toxins; and demyelinated lesions of the nervous system, in which a
XX portion of the nervous system is destroyed or injured by a demyelinating
XX disease e.g. multiple sclerosis, HIV-associated myelopathy, transverse
XX myelopathy of various etiologies, progressive multifocal
XX leukoencephalopathy or central pontine myelinolysis; or lesions of the
XX central or peripheral nervous systems. In addition, agents which promote
XX Nr-CAM function can be promoted to increase growth of animals (e.g. cows,

CC horses, pigs, goats, deer, chickens) and plants (particularly edible
CC plants, e.g. tomatoes, melons, lettuce, carrots, potatoes, and other
CC vegetables), particularly those that are food or material sources. They
CC can also be used in vitro e.g. to expand cells e.g. stem cells,
CC progenitor cells, muscle cells, fibroblasts, or liver cells to grow
CC cells/tissue in vitro prior to administration to a patient. The products
CC can also be used for detection, diagnosis and production of animal
CC models. The present sequence represents a previously cloned human Nr-CAM
CC gene (accn no: AA055258) fragment.

CC Sequence 38 BP; 12 A; 5 C; 7 G; 14 T; 0 other;

Query Match 0.9%; Score 38; DB 21; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4097 tctcatcattgaacattatggtagagattatttc 4134
Db 1 tctcatcattgaacattatggtagagattatttc 38

RESULT 6

AAC14618
ID AAC14618 standard; cDNA; 97 BP.

AC14618;

06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 18693.

Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.

Homo sapiens.

EPI033401-A2.

06-SEP-2000.

21-FEB-2000; 2000EP-0200610.

26-FEB-1999; 99US-0122487.

(GEST) GENSET.

Dumas Milne Edwards J, Duclert A, Giordano J;

WPI; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for
obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
diagnostic, forensic, gene therapy and chromosome mapping procedures -
Claim 1; SEQ ID 18693; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from
mRNAs encoding secreted proteins. No ORF has yet been conclusively
identified within the present sequence. The 5' ESTs were prepared from
total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
sequences usually correspond mainly to the 3' untranslated region (UTR)
of the mRNA because they are often obtained from oligo-dT primed cDNA
libraries. Such ESTs are not well suited for isolating cDNA sequences
derived from the 5' ends of mRNAs and even in those cases where longer
cDNA sequences have been obtained, the full 5' UTR is rarely included.
5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
in diagnostic, forensic, gene therapy and chromosome mapping procedures.
They are used to obtain upstream regulatory sequences and to design
expression and secretion vectors.

Sequence 97 BP; 43 A; 8 C; 28 G; 14 T; 4 other;

Query Match 0.7%; Score 28; DB 21; Length 97;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 42; Conservative 3; Mismatches 25; Indels 0; Gaps 0;

OY 3853 aaaaagaagatagtgagacagcctgtgactatgaggaagggttaatgacagtc 3912
Db 21 aatgaagaagaacaaacagacagcctgtgactatgaggaagggttaatgacagtc 80

OY 3913 aatgagatg 3922
Db 81 gatgagatg 90

RESULT 7

AAV40897/C
ID AAV40897 standard; DNA; 29 BP.

AAV40897.

25-SEP-1998 (first entry)

Probe for coding sequence of clone CO722.1.

Human; nutritional supplement; cell proliferation/differentiation;
cytokine; immunostimulant; immunosuppressant; hematopoiesis regulator;
receptor/ligand activity; cadherin/tumour invasion suppressor; probe;
anti-inflammatory; tumour inhibitor; clone CO722.1; ss.

Synthetic.

Homo sapiens.

WO9824905-A2.

11-JUN-1998.

05-DEC-1997; 97WO-US22211.

03-DEC-1997; 97US-0984516.

06-DEC-1996; 96US-0762216.

(GEMV) GENETICS INST INC.

Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
Racie LA, Spaulding V, Treacy M;

WPI; 1998-333324/29.

New isolated polynucleotides encoding secreted polypeptides -
Isolated from a human foetal kidney cDNA library, a human adult
blood cDNA library or a human adult brain cDNA library
Disclosure; Page 93; 109pp; English.

This sequence represents a probe for the coding sequence of clone
CO722.1 of the invention. The clone was isolated from a human adult
brain cDNA library. The DNAs and proteins can be used as nutritional
sources or supplements, or may exhibit cytokine and cell
proliferation/differentiation activity, immune stimulating or suppressing
activity, hematopoiesis regulation activity, receptor/ligand activity,
anti-inflammatory activity, cadherin/tumour invasion suppressor activity,
tumour inhibition activity or other activities.

Sequence 29 BP; 7 A; 9 C; 4 G; 8 T; 1 other;

Query Match 0.7%; Score 28; DB 19; Length 29;
Best Local Similarity 96.6%; Pred. No. 3e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 75 aaggaattcagtgctgtgagcttcagcag 103
|||||

Db 29 AAGGAATTCAGTGTGTGAGTCTCAGCNG 1

RESULT 8

ID AAA64165/C

AC AAA64165;

XX 20-DEC-2000 (first entry)

XX Probe used to isolate cDNA encoding secreted protein clone CO722.1.

XX Human; secreted protein; immune deficiency; infectious disease;
 KW tissue growth; wound healing; tissue repair; burn; incision; ulcer;
 KW osteoporosis; osteoarthritis; periodontal disease; tooth repair;
 KW nervous system disorder; angiogenic cytokine damage; fibrosis; fertility;
 KW reperfusion injury; systemic cytokine damage; contraceptive;
 KW thrombolytic; coagulation disorder; anti-inflammatory activity;
 KW inflammatory condition; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX modified_base 2
 XX /*tag= a
 XX /note= "biotinylated phosphoramidite residue"

XX WO2000592-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-0S04731.

XX 24-FEB-1999; 99US-0256938.

XX (GENY) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

XX Merberg D, Treacy M, Bowman MR, Spaulding V;

XX WPI: 2000-55839/51.

XX New secreted polypeptides and nucleic acids encoding them used for
 PT treating various anemias, bone, cartilage, tendon, ligament and/or
 PT nerve tissue or regeneration, contraceptives, and nutritional
 PT supplements

XX Disclosure; Page 115; 119pp; English.

XX The present sequence represents a probe for cDNA encoding a human
 CC secreted protein. The polypeptides may be used in the treatment of
 CC various immune deficiencies and disorders, and to treat infectious
 CC diseases caused by viral, bacterial, fungal or other infections. The
 CC polypeptides are also used in compositions for bone, cartilage, tendon,
 CC ligament and/or nerve tissue growth or regeneration, for wound healing
 CC and tissue repair and replacement, and in the treatment of burns,
 CC incisions and ulcers. The protein is used in the treatment of
 CC osteoporosis or osteoarthritis, periodontal disease and other tooth
 CC repair processes, and nervous system disorders. They also exhibit
 CC angiogenic activity and protect, regenerate and treat lung or liver
 CC fibrosis, reperfusion injury in various tissues, and conditions
 CC resulting from systemic cytokine damage. They promote or inhibit tissue
 CC differentiation and are used as contraceptive and to enhance fertility.
 CC They also have a hemostatic or thrombolytic activity and can be used
 CC to treat various coagulation disorders. They also have an
 CC anti-inflammatory activity and can be used to treat inflammatory
 CC conditions.

XX Sequence 29 BP; 7 A; 9 C; 4 G; 8 T; 1 other;

Query Match 0.7%; Score 28; DB 21; Length 29;

Best Local Similarity 96.6%; Pred. No. 3e+02;

Oy 75 aaggaatcagtggtgagtcacag 103

Db 29 AAGGAATTCAGTGTGTGAGTCTCAGCNG 1

RESULT 9

ID AAF98540/C

AC AAF98540;

XX 07-JUN-2001 (first entry)

XX Human cDNA clone CO722.1 specific probe SEQ ID 250.

XX Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 KW haematopoiesis; probe.

XX Homo sapiens.

XX WO200119988-A1.

XX 22-MAR-2001.

XX 14-SEP-2000; 2000WO-US25135.

XX 17-SEP-1999; 99US-0398829.

XX (GENY) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

XX Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

XX WPI: 2001-244801/25.

XX Isolated nucleic acids encoding polypeptides, useful for modulating
 PT e.g. cytokine and cell proliferation/differentiation activity, the
 PT immune system and hematopoiesis regulating activity -
 PT

XX Disclosure; Page 540; 557pp; English.

XX Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic
 CC activity; receptor/ligand activity; anti-inflammatory activity;
 CC haematopoiesis activity; cadherin/tumour suppressor activity; and/or
 CC tumour inhibition activity. Included in the invention are probes
 CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
 CC encoding the secreted proteins.

XX Sequence 29 BP; 7 A; 9 C; 4 G; 8 T; 1 other;

Query Match 0.7%; Score 28; DB 22; Length 29;
 Best Local Similarity 96.6%; Pred. No. 3e+02;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 75 aaggaatcagtggtgagtcacag 103

Db 29 AAGGAATTCAGTGTGTGAGTCTCAGCNG 1

ID	AAZ38180/C	AAZ38180 standard; DNA; 50 BP.
XX	AAZ38180.	
XX	14-FEB-2000 (first entry)	
XX	Human Nr-CAM gene specific primer BT307.	
XX	Nr-CAM; neuron-glia-related cell adhesion molecule; cell proliferation;	
XX	tumorigenesis; malignancy; cancer; leukemia; hyperproliferative disorder;	
XX	degenerative disorder; growth deficiency; trauma; wound; tumor; diabetes;	
XX	systemic lupus erythematosus; demyelinating disease; PCR primer; ss.	
XX	Synthetic.	
XX	Homo sapiens.	
XX	MO9955380-A1.	
XX	04-NOV-1999.	
XX	27-APR-1999; 99MO-US09039.	
XX	27-APR-1998; 98US-0083152.	
XX	14-DEC-1998; 98US-0112098.	
XX	(PACI-) PACIFIC NORTHWEST CANCER FOUND.	
XX	Murphy GP, Boynton AL, Sehgal A;	
XX	WPI: 2000-023268/02.	
XX	Use of neuron-glia-related cell adhesion molecule for developing agents	
XX	for the diagnosis and treatment of e.g. cancers, hyperproliferative	
XX	disorders, growth deficiencies, degenerative disorders, trauma or	
XX	wounds	
XX	Examples; Page 124; 183pp; English.	
XX	The invention relates to the use of neuron-glia-related cell adhesion	
XX	molecule (Nr-CAM) as a marker for diagnosing, treating, inhibiting or	
XX	preventing disorders involving cell proliferation. An antisense nucleic	
XX	acid complementary to at least a portion of an RNA transcript of a	
XX	Nr-CAM gene can be used to inhibit hyperproliferation of a tumor cell,	
XX	for the treatment of tumorigenesis. Agents which inhibit and promote	
XX	Nr-CAM function can be used for the treatment of various diseases and	
XX	disorders (see AAZ38152 for a detailed description). The products can	
XX	also be used for detection, diagnosis and production of animal models.	
XX	Sequences AAZ38179-80 represent primers specific for the human Nr-CAM	
XX	gene.	
XX	Sequence 50 BP; 15 A; 11 C; 11 G; 13 T; 0 other;	
XX	50	
XX	Query Match	0.6%; Score 26.4; DB 21; Length 50;
XX	Best Local Similarity	83.3%; Pred. No. 1.3e+03;
XX	Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0	
XX	1399 gatatcagtgcaatgcctctaataatgatgat 1434	
XX		
XX	50 GTATGGGATCCCAATGCTCTATGATGATGATAT 15	
XX	RESULT 11	
XX	AAAT44495/C	
XX	AAAT44495 standard; DNA; 82 BP.	
XX	AAAT44495:	
XX	22-FEB-1997 (first entry)	

DE	Murine p57KIP2 gene translation initiation region.
XX	
KW	Cyclin-dependent kinase inhibitor; CDK; CDI; p57KIP2; cell cycle;
KM	cancer; hyperplasia; ulcer; hyperproliferation; hypoproliferation;
KW	diagnosis; gene therapy; ss.
XX	
OS	Mus sp.
XX	
FH	location/Qualifiers
FT	1..15
FT	/tag= a
FT	/note= "3' end of exon sequence"
FT	16...28
FT	/tag= b
FT	/note= "base n at position 22 denotes an approx. 200 bp intronic sequence not provided in Fig 4"
FT	exon
FT	29..82
FT	/tag= c
FT	/codon_start= 39
FT	/note= "there is an alternative codon start site at position 78 for use with B and B' splicing events"
FT	misc_feature
FT	29
FT	/tag= d
FT	/label= A
FT	/note= "p57 acceptor site A"
FT	67
FT	/tag= e
FT	/label= B
FT	/note= "alternative acceptor site B"
FT	70
FT	/tag= f
FT	/label= B'
FT	/note= "alternative acceptor site B'"
PN	WO9631534-A1.
XX	
PD	10-OCT-1996.
XX	
PF	03-APR-1996; 96WO-US04563.
XX	
PR	03-APR-1995; 95US-0415655.
XX	
PA	(SLOAN) SLOAN KETTERING INST CANCER RES.
PI	Lee M, Massague J;
XX	
DR	WPI; 1996-464971/46.
XX	
P-PSDB; AA001438.	
XX	
PT	Mammalian p57-KIP2 and related DNA - used to develop prods. useful for diagnosis and treatment of hyper- and hypo-proliferative disorders
XX	
PS	Disclosure; Fig 4; 98pp; English.
XX	
CC	3 Distinct cDNA clones (AA001438-98) are derived from genomic DNA (AA001438) in the translation start region of the murine gene (see also AA001438) coding for cyclin-dependent kinase inhibitor p57KIP2 (AA001438). These result from splicing at position A, leading to the full-length (348-amino acid) protein having the N-terminal sequence shown in AA001438, or alternative splicing at positions B or B', resulting in a 335-amino acid product, designated p57KIP2B. The intron sequence in the genomic DNA was identified by PCR analysis (see also AA001438-01).
XX	
SQ	Sequence 82 BP; 21 A; 27 C; 21 G; 12 T; 1 other;
Query Match	0.6%; Score 26; DB 17; Length 82;
Best Local Similarity	58.7%; Pred. No. 2.3e+03;
Matches 44; Conservative	0; Mismatches 31; Indels 0; Gaps 0;


```

XX OS Synthetic.
XX XX
XX Key Location/Qualifiers
XX FH 10..26
XX FT promoter /tag= a
XX FT /label= T7_promoter
XX FT 5'UTR 27..64
XX FT /tag= b
XX FT /label= UTL_from_AMV
XX PN WO9207949-A.
XX XX
XX PD 14-MAY-1992.
XX XX
XX PF 05-NOV-1991; 91WO-US08291.
XX XX
XX PR 05-NOV-1990; 90US-0609318.
XX XX
XX PA (USSA ) US SEC OF ARMY.
XX PI Kaln KC, Lanar DE;
XX XX
XX DR WPI: 1992-183684/22.
XX XX
XX PT Protein in vitro prodn. for efficient transcription - avoids
XX FT cloning of deoxyribonucleic acid by expression polymerase chain
XX FT reaction for translation
XX XX
XX PS Disclosure; Fig 2; 37pp; English.
XX XX
CC The sequences given in AAQ24812 - AAQ24815 are universal promoter (UP)
CC sequences which contain a double stranded RNA transcription
CC promoter, an untranslated leader sequence enhancing translation
CC activity followed by three codons, the first of which encodes Met.
CC These UP's can be used in a process described as expression
CC polymerase chain reaction (E-PCR). The active polymerase binding
CC site used in this invention is the one for viral T7 RNA polymerase,
CC however, any promoter site may be used that corresponds to the RNA
CC polymerase that will be employed for the transcription of the DNA.
CC Promoter sites for suitable polymerases that could be used are
CC those for the SP6 polymerase, the T3 or T4 phage polymerases or the
CC ghl promoter. The untranslated leader (UTL) sequence between the T7
CC promoter and the initial ATG codon is derived from the coat protein
CC mRNA of the alfalfa mosaic virus (AMV). In vitro translation of mRNA
CC is often dependant on the presence of, and the characteristics of, an
CC UTL sequence 5' to the initiation codon. It has been shown that
CC replacement of a genes native UTL with the AMV UTL can increase
CC translational efficiency by as much as 35-fold. Other UTL sequences
CC may be substituted for this AMV UTL.
XX XX
SQ Sequence 71 BP; 19 A; 16 C; 7 G; 29 T; 0 other;
Query Match 0.6%; Score 25.8; DB 13; Length 71;
Best Local Similarity 63.9%; Pred. NO. 2.4e+03;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 626 ttggtaccacacacataatttggatgataatctcttcaagaacttcacaa 685
DB 7 ttctaatagcactcactataggttttatttatttcttcaataacttcacat 66
QY 686 g 686
DB 67 g 67
RESULT 15
AAQ24815
ID AAQ24815 standard; DNA; 73 BP.
XX AC
XX AAQ24815;
XX XX

```

```

DT 19-NOV-1992 (first entry)
XX DE Universal promoter-4.
XX XX
XX UP; untranslated leader sequence; E-PCR; T7 RNA polymerase; SP6;
XX KW T3; T4; ghl; alfalfa mosaic virus; ds.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT 10..26
XX FT promoter /tag= a
XX FT /label= T7_promoter
XX FT 5'UTR 27..64
XX FT /tag= b
XX FT /label= UTL_from_AMV
XX PN WO9207949-A.
XX XX
XX PD 14-MAY-1992.
XX XX
XX PF 05-NOV-1991; 91WO-US08291.
XX XX
XX PR 05-NOV-1990; 90US-0609318.
XX XX
XX PA (USSA ) US SEC OF ARMY.
XX PI Kaln KC, Lanar DE;
XX XX
XX DR WPI: 1992-183684/22.
XX XX
XX PT Protein in vitro prodn. for efficient transcription - avoids
XX FT cloning of deoxyribonucleic acid by expression polymerase chain
XX FT reaction for translation
XX XX
XX PS Disclosure; Fig 4; 37pp; English.
XX XX
CC The sequences given in AAQ24812 - AAQ24815 are universal promoter (UP)
CC sequences which contain a double stranded RNA transcription
CC promoter, an untranslated leader sequence enhancing translation
CC activity followed by three codons, the first of which encodes Met.
CC These UP's can be used in a process described as expression
CC polymerase chain reaction (E-PCR). The active polymerase binding
CC site used in this invention is the one for viral T7 RNA polymerase,
CC however, any promoter site may be used that corresponds to the RNA
CC polymerase that will be employed for the transcription of the DNA.
CC Promoter sites for suitable polymerases that could be used are
CC those for the SP6 polymerase, the T3 or T4 phage polymerases or the
CC ghl promoter. The untranslated leader (UTL) sequence between the T7
CC promoter and the initial ATG codon is derived from the coat protein
CC mRNA of the alfalfa mosaic virus (AMV). In vitro translation of mRNA
CC is often dependant on the presence of, and the characteristics of, an
CC UTL sequence 5' to the initiation codon. It has been shown that
CC replacement of a genes native UTL with the AMV UTL can increase
CC translational efficiency by as much as 35-fold. Other UTL sequences
CC may be substituted for this AMV UTL.
XX XX
SQ Sequence 73 BP; 19 A; 17 C; 8 G; 29 T; 0 other;
Query Match 0.6%; Score 25.8; DB 13; Length 73;
Best Local Similarity 63.9%; Pred. NO. 2.4e+03;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 626 ttggtaccacacacataatttggatgataatctcttcaagaacttcacaa 685
DB 7 ttctaatagcactcactataggttttatttatttcttcaataacttcacat 66
QY 686 g 686
DB 67 g 67

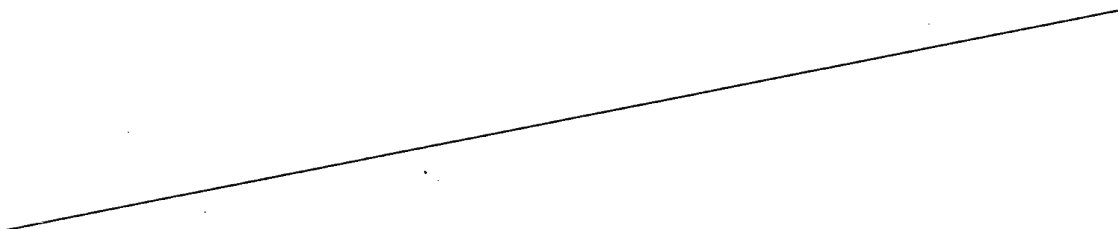
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Search completed: August 13, 2002, 22:49:51
Job time 8725 sec

us-09-301-380-1.img



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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 19:38:44 ; Search time 82.1 Seconds
(without alignments)
12368.440 Million cell updates/sec

Title: US-09-301-380-1
Perfect score: 4134
Sequence: 1 ctcaaaagttcccgcatga.....tggtagagatattttc 4134

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 576162

Minimum DB seq length: 15
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgnt2_6/prodata/1/lna/5B.COMB.seq:*
3: /cgnt2_6/prodata/1/lna/6A.COMB.seq:*
4: /cgnt2_6/prodata/1/lna/6B.COMB.seq:*
5: /cgnt2_6/prodata/1/lna/PCRTUS.COMB.seq:*
6: /cgnt2_6/prodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	0.6	70	1	US-08-441-430-9
2	24	0.6	100	4	US-09-564-805-23
3	23.6	0.6	67	4	US-09-025-769B-83
4	23.4	0.6	66	2	US-08-709-874A-15
5	23.4	0.6	66	4	US-09-104-382-15
6	23	0.6	60	3	US-08-415-655-10
7	22.8	0.6	63	1	US-08-386-495-1
8	22.8	0.6	63	5	PCR-US96-02331-1
9	22.8	0.6	78	1	US-08-446-102-1
10	22.8	0.6	78	1	US-08-446-102-2
11	22.8	0.6	78	4	US-08-617-010C-15
12	22.8	0.6	78	4	US-09-566-591-15
13	22.8	0.6	100	4	US-09-242-690A-58
14	22.6	0.5	94	1	US-08-105-483-447
15	22.6	0.5	94	1	US-08-105-483-448
16	22.6	0.5	94	1	US-08-709-209-447
17	22.6	0.5	94	1	US-08-709-209-448
18	22.6	0.5	94	1	US-08-303-275-159
19	22.6	0.5	94	1	US-08-303-275-160
20	22.6	0.5	94	1	US-08-458-101-447
21	22.6	0.5	94	1	US-08-458-101-448
22	22.6	0.5	100	3	US-08-836-561-61
23	22.4	0.5	78	4	US-09-240-078-43
24	22.2	0.5	77	1	US-08-242-663A-3
25	22.2	0.5	77	5	PCR-US95-06132-3
26	22.2	0.5	79	2	US-08-184-009-158
27	22.2	0.5	79	2	US-08-458-356-158

C	28	22.2	0.5	79	4	US-08-460-736-158	Sequence 158, App
	29	22.2	0.5	84	1	US-08-182-175A-27	Sequence 27, App1
	30	22.2	0.5	84	1	US-08-474-633A-68	Sequence 68, App1
	31	22.2	0.5	84	5	PCR-US92-06412-27	Sequence 27, App1
	32	22.2	0.5	95	2	US-08-332-766A-41	Sequence 41, App1
	33	22.2	0.5	60	1	US-08-153-848-10	Sequence 10, App1
	34	22.2	0.5	60	3	US-09-299-843A-10	Sequence 10, App1
	35	22.2	0.5	60	4	US-09-088-337B-10	Sequence 10, App1
	36	22.2	0.5	60	5	PCR-US93-11153-10	Sequence 10, App1
	37	22.2	0.5	90	1	US-08-513-846-2	Sequence 2, App1
	38	22.2	0.5	90	1	US-08-513-846-18	Sequence 18, App1
	39	22.2	0.5	93	2	US-08-105-989-12	Sequence 12, App1
	40	22.2	0.5	93	3	US-09-138-922-12	Sequence 12, App1
C	41	21.8	0.5	56	1	US-08-441-430-25	Sequence 25, App1
C	42	21.8	0.5	76	3	US-08-284-516C-22	Sequence 22, App1
C	43	21.8	0.5	81	1	US-08-238-863-42	Sequence 42, App1
C	44	21.8	0.5	81	1	US-08-443-407-42	Sequence 42, App1
C	45	21.8	0.5	81	5	PCR-US95-05600-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-08-441-430-9
Sequence 9, Application US/08441430
Patent No. 5681942
GENERAL INFORMATION:
APPLICANT: Buchwald, Manuel
APPLICANT: Strathdee, Craig A.
APPLICANT: Wevrick, Rachel
APPLICANT: Mathew, Christopher George Porter
TITLE OF INVENTION: Fancorn Anemia Type C Gene
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Klarquist, Sparkman, Campbell, Leigh &
ADDRESSEE: Whinston, LLP
STREET: 121 S.W. Salmon, Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3+1-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1/ASCII Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,430
FILING DATE: May 15, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/876,285
FILING DATE: April 29, 1992
APPLICATION NUMBER: U.S. 07/918,313
FILING DATE: July 21, 1992
APPLICATION NUMBER: U.S. 08/003,963
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley, Esq.
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 3812-42824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double stranded
TOPOLOGY: Linear
MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-441-430-9

Query Match 0.6%; Score 25; DB 1; Length 70;
Best Local Similarity 61.5%; Pred. No. 5.2e+02;
Matches 40; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 3449 aaattgtaattgttcctgagcttcttgggttaagggtcctaagccaggaacagcat 3508
DB 4 ACAGAGTAATCTGCTCGACACTCTTGAATTAATGATTAATTAAGAGTCTGCTT 63

QY 3509 acaaa 3513
DB 64 AAAAA 68

RESULT 2
US-09-564-805-23/C
Sequence 23, Application US/09564805
Patent No. 6333403

GENERAL INFORMATION:
APPLICANT: Tavligian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564, 805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107, 468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434, 382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 100
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(100)
OTHER INFORMATION: exon 20
US-09-564-805-23

Query Match 0.6%; Score 24; DB 4; Length 100;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 48; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 3297 caaagttcaagcgtgtaaccagatcagacacttactctgtagctgtagaccta 3356
DB 94 CAATTCATGCTTGGCAACGAGCATGATCAATCTTCCATCGACGACATGAGATCTC 35

QY 3357 tgccaataatcagttgggaatatgagga 3384
DB 34 AGCCCTTCTCTGAAGGCAATTTGGCAGGA 7

RESULT 3
US-09-025-769B-83/C
Sequence 83, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide Libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025, 769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic oligonucleotide"

US-09-025-769B-83

Query Match 0.6%; Score 23.6; DB 4; Length 67;
Best Local Similarity 76.3%; Pred. No. 1.3e+03;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1228 ctgtcccccagagagatgagaccttgatctgagagc 1265
DB 39 CTGTCTCCGGCGGACGTGCGACCTCGAGCTCGACAGGC 2

RESULT 4
US-08-709-874A-15
Sequence 15, Application US/08709874A
Patent No. 5854040

GENERAL INFORMATION:
APPLICANT: Ozaki, Akio
APPLICANT: Mori, Hideo
APPLICANT: Shibasaki, Takeshi
APPLICANT: Ando, Katsuhiko
APPLICANT: Chiba, Shigeru
TITLE OF INVENTION: Process for Producing
NUMBER OF SEQUENCES: 29
TITLE OF INVENTION: Trans-4-Hydroxy-L-Proline
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS, LLP
STREET: 1300 NORTH SEVENTEENTH STREET
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22209

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,874A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/301,653
FILING DATE: 07-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,554
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-709-874A-15

Query Match 0.6%; Score 23.4; DB 2; Length 66;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 3266 ctggtatcttcaccctgtagtgcagggcaaaagttcaagctgtaataaccaggatca 3325
DB 1 CCGGAATTCTGCTGACTTCACGGCGGCCAGCCCATCTTCATCAGCAGATAGCCCGCTTC 60

QY 3326 gcaat 3330
DB 61 ACGAT 65

RESULT 5
US-09-104-382-15
Sequence 15, Application US/09104382
Patent No. 624231
GENERAL INFORMATION:
APPLICANT: Ozaki, Akio
APPLICANT: Mori, Hideo
APPLICANT: Shibasaki, Takeshi
APPLICANT: Ando, Katsuhiko
APPLICANT: Chiba, Shigeru
TITLE OF INVENTION: Process for Producing
TITLE OF INVENTION: Trans-4-Hydroxy-L-Proline
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS, LLP
STREET: 1300 NORTH SEVENTEENTH STREET
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,382
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/709,874
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: 08/301,653
FILING DATE: 07-SEP-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,554
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-09-104-382-15

Query Match 0.6%; Score 23.4; DB 4; Length 66;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 3266 ctggtatcttcaccctgtagtgcagggcaaaagttcaagctgtaataaccaggatca 3325
DB 1 CCGGAATTCTGCTGACTTCACGGCGGCCAGCCCATCTTCATCAGCAGATAGCCCGCTTC 60

QY 3326 gcaat 3330
DB 61 ACGAT 65

RESULT 6
US-08-415-655-10/C
Sequence 10, Application US/08415655
Patent No. 6025480
GENERAL INFORMATION:
APPLICANT: Massage, Joan
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: P73KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
TITLE OF INVENTION: SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/47418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-415-655-10

Query Match

Best Local Similarity 0.6%; Score 23; DB 3; Length 60;
Matches 35; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

1840 tccctcactgctcgtgctgaagacacagaggaactggcccaagtatgaagt 1894
Db 59 TCCATGCTGTTCTGCTGCGGAGGTACAGTCGACATGCCCATGTCGAAGCT 5

RESULT 7

US-08-386-495-1/C
Sequence 1, Application US/08386495
Patent No. 5753434

GENERAL INFORMATION:

APPLICANT: Ryner, Lisa C.
APPLICANT: Baker, Bruce S.
APPLICANT: Masserman, Steven A.
APPLICANT: Castillon, Diego H.
TITLE OF INVENTION: Methods and Compositions for Altering
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,495
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 3x repeat probe
US-08-386-495-1

Query Match

Best Local Similarity 0.6%; Score 22.8; DB 1; Length 63;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1608 tgaagatattatglttaccatgaagaatggaacttggaaatcaaatg 1657
Db 54 TGAAGATGATCTATGTGATTGAAGATGGATCTATGTGATTGAAGATG 5

RESULT 8

PCT-US96-02331-1/C
Sequence 1, Application PC/TUS9602331

GENERAL INFORMATION:

APPLICANT: The Board of Trustees of the Leland Stanford Junior
APPLICANT: University
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Methods and Compositions for Altering
TITLE OF INVENTION: Sexual Behavior
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/02331
FILING DATE: 09-FEB-1996
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/386,495
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0153.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 3x repeat probe
PCT-US96-02331-1

Query Match

Best Local Similarity 0.6%; Score 22.8; DB 5; Length 63;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1608 tgaagatattatglttaccatgaagaatggaacttggaaatcaaatg 1657
Db 54 TGAAGATGATCTATGTGATTGAAGATGGATCTATGTGATTGAAGATG 5

RESULT 9

US-08-446-102-1/C

Sequence 1, Application US/08446102

GENERAL INFORMATION:

APPLICANT: SMITH, Cassandra L.
APPLICANT: VAAR, Ron
APPLICANT: SZAFRANSKI, Przemyslaw
APPLICANT: CANTOR, Charles R.

APPLICATION NUMBER: 08/178,216
FILING DATE: 06-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/001,323
FILING DATE: 07-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-617-010C-15

Query Match
Best Local Similarity 59.1%; Score 22.8; DB 4; Length 78;
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1994 ccagcgcgtgtctagcgtgtgtctctaccacccacccacccgttaccgattgc 2053
Db 10 CCAGGATTCGGTTAGCGCTGACTGCTGCTGCTGCTGCTGATGATCGACGCAAT 69

QY 2054 caatc 2059
Db 70 CAGATC 75

RESULT 12
US-09-566-591-15
Sequence 15, Application US/09566591
Patent No. 6238871
GENERAL INFORMATION:
APPLICANT: Hubert K'ster
TITLE OF INVENTION: DNA SEQUENCING BY MASS SPECTROMETRY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehtman White & McAuillife
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037-9103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/566,591
FILING DATE: 08-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/617,010
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: 08/178,216
FILING DATE: 06-JAN-1994
APPLICATION NUMBER: 08/001,323
FILING DATE: 07-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2012B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8400

TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-566-591-15

Query Match
Best Local Similarity 59.1%; Score 22.8; DB 4; Length 78;
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1994 ccagcgcgtgtctagcgtgtgtctctaccacccacccacccgttaccgattgc 2053
Db 10 CCAGGATTCGGTTAGCGCTGACTGCTGCTGCTGCTGCTGATGATCGACGCAAT 69

QY 2054 caatc 2059
Db 70 CAGATC 75

RESULT 13
US-09-242-690A-58
Sequence 58, Application US/09242690A
Patent No. 6284534
GENERAL INFORMATION:
APPLICANT: KONDO, KEIJI
TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
FILE REFERENCE: 049441/0118
CURRENT APPLICATION NUMBER: US/09/242,690A
CURRENT FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: PCT/JP97/02924
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: JP 8/241062
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 58
LENGTH: 100
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-242-690A-58

Query Match
Best Local Similarity 56.8%; Score 22.8; DB 4; Length 100;
Matches 42; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2519 atgtatccaatatatgtctcagcgacgacaccccttgcctaccatcgtatgaattc 2578
Db 1 aagtcagcagccttaagattccctcacccctaccctgttaccgactgattcgtggttt 60

QY 2579 aggcctgaatgac 2592
Db 61 tggatgttaacgac 74

RESULT 14
US-08-105-483-447
Sequence 447, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE

TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 447:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-447

Query Match 0.5%; Score 22.6; DB 1; Length 94;
Best Local Similarity 54.1%; Pred. No. 3.2e+03;
Matches 46; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 619 ccccaattgattaccaccataataatttgatgataattcccttcaagaactt 678
DB 4 CCTCCTTTAGAAACACGAGATATTATTCTTGTGGGATCAATCTTAAACCTCCT 63
QY 679 ccacaagtggagaggttctcaag 703
DB 64 TTTAGAAAGATAGATATTGAAG 88

RESULT 15
US-08-105-483-448/c
Sequence 448, Application US/08105483
Patent No. 3494807
GENERAL INFORMATION:
APPLICANT: Paolelli, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 448:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-448

Query Match 0.5%; Score 22.6; DB 1; Length 94;
Best Local Similarity 54.1%; Pred. No. 3.2e+03;
Matches 46; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 619 ccccaattgattaccaccataataatttgatgataattcccttcaagaactt 678
DB 91 CCTCCTTTAGAAACACGAGATATTATTCTTGTGGGATCAATCTTAAACCTCCT 32
QY 679 ccacaagtggagaggttctcaag 703
DB 31 TTTAGAAAGATAGATATTGAAG 7

Search completed: August 13, 2002, 22:42:33
Job time: 11029 sec

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Result No.	Score	Query Match	Length	DB	ID	Description
1	28.8	0.7	85	9	A1096387	A1096387 gb91.f10.x
2	27.6	0.7	88	9	A1007269	A1007269 ua33h03.x
3	26.6	0.6	84	10	BE322578	BE322578 NF006E055
4	26.4	0.6	100	9	AW101101	AW101101 sg74a07.y
5	26	0.6	71	10	D78209	D78209 D78209.EST
6	26	0.6	83	12	TA293D120	TA293D120 T. brucei
7	26	0.6	92	9	AA470870	AA470870 nei19g03.s
8	26	0.6	93	10	BG7966297	BG7966297 UTMW_SM4
9	26	0.6	95	10	BE324593	BE324593 NF014E055
10	26	0.6	96	10	W03279	W03279 za36c11.r1
11	26	0.6	100	9	AW845547	AW845547 MRI-C7005
12	26	0.6	100	10	D45290	D45290 HUMHG2360.F
13	25.8	0.6	71	12	AZ826637	AZ826637 2M0102X080
14	25.8	0.6	85	10	BE289162	BE289162 6010892755
15	25.8	0.6	99	12	FR0023001	FR0023001 F. tularensis
16	25.8	0.6	100	10	BE092347	BE092347 KKA-TN014
17	25.4	0.6	95	10	B1654803	B1654803 B63281144

C	18	25.2	0.6	98	9	AA716301	zh28e12.s
C	19	25.2	0.6	100	9	AV001666	AV001666 zh001666
C	20	25	0.6	87	12	FR0010708	AL001980 F. rubritype
C	21	25	0.6	100	10	Bg221902	Bg221902 RST4179
C	22	24.8	0.6	64	10	BE636385	BE636385 SMOVAMCAQ
C	23	24.8	0.6	73	10	M88076	M88076 mf67e10..r1
C	24	24.8	0.6	80	9	AM246647	AM246647 2821633..3
C	25	24.8	0.6	84	9	AM675386	AM675386 DB45909.y
C	26	24.8	0.6	94	10	RS1717	RS1177 Y977F06..r1
C	27	24.8	0.6	95	9	AI153902	AI153902 udc50e04..r
C	28	24.8	0.6	96	12	AF166318	AF166318 AF166318
C	29	24.6	0.6	99	10	BF378532	BF378532 OY1-UM003
C	30	24.6	0.6	79	9	AA670839	AA670839 vS30e06..r
C	31	24.6	0.6	98	12	A26835091	A26835091 ZM0129G11
C	32	24.6	0.6	97	9	AI628325	AI628325 ts36f01..x
C	33	24.6	0.6	97	9	AA232334	AA232334 czr27b04..r
C	34	24.6	0.6	97	9	AW395938	AW395938 sh07f05.y
C	35	24.4	0.6	71	12	A2336643	A2336643 IM0068A14
C	36	24.4	0.6	73	10	BM053420	BM053420 i66a607.y
C	37	24.4	0.6	78	9	AA935490	AA935490 n253c02.s
C	38	24.4	0.6	85	9	AI477927	AI477927 fbd49b10..x
C	39	24.4	0.6	88	9	AA523959	AA523959 ny26g01.s
C	40	24.4	0.6	94	9	AW496789	AW496789 ltg Neuro
C	41	24.4	0.6	95	12	A2468419	A2468419 IM0281K19
C	42	24.4	0.6	100	9	AA237743	AA237743 mx77a06..r
C	43	24.2	0.6	64	9	AW599941	AW599941 SMOVARPCAP
C	44	24.2	0.6	87	10	BI493713	BI493713 dft104F06.
C	45	24.2	0.6	88	12	A2784747	A2784747 ZM0027B09

ALIGNMENTS

RESULT

LOCUS	A1096387	85 bp	mRNA	linear	EST 26-OCT-1998
DEFINITION	qb91f10.x1 Soares_fetal_heart_NbH19W Homo sapiens cdna clone				

```

IMAGE:1707499 3' similar to SW:FSA_BOVIN P50291 FOLLICULASTATIN
PRECURSOR ;, mRNA sequence.
1706567

```

ACCESSION	AI09638/
VERSION	AI096387.1
KEYWORDS	GT:3446298
	ECM

KEYWORDS	EST.
SOURCE	human.
ORGANISM	human.

ORGANISM
nomio sapientis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthioria; Primates; Carnivora; Insectivora; Homo

REFERENCE
AUTHORS
1 (bases 1 to 85)
MCT-CGAP <http://www.mct-cgap.net>

TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D

Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNC; contact the

IMAGE Consortium. (infoimage.lnl.gov) for further information.
Trace considered overall poor quality

Insert Length: 1428 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham

FEATURES	High quality sequence stop: 1
Location/Qualifiers	Location/Qualifiers

```
source
1. .85
/organism="Homo sapiens"
```

```

/db_xref="taxon:9606"
/clone="IMAGE:1707499"
(clone 14="Germes 6649") parent="bnu104"

```

```

/clone_id=soates_delta_nearc_nohh19w
/sex="unknown"
/day stage="10 weeks"

```

```

new_stage= 15 weeks
lab_host="DH10B (ampicillin resistant)"
/notes= heart: Vector; RT773D (Pha

```

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'

double-stranded cDNA was size selected, ligated to Eco RI

D _b	94	TGTGGNAAATCTCGAACAANNANNAAGSAGTACCCCTNNTCACNTGCTTAATATYTCGNA	35
O _y	3183	ataaaagtttattcttcatagcacaaacat	3211
	34	ATTNTNMANANTGAGTTTATATATCAINCAT	6

RESULT	11
AW845547/c	
LOCUS	100 bp
DEFINITION	mRNA linear
ACCESSION	KM1-CTO058-931199-003-d02 CTO058 Homo sapiens CDNA, mRNA sequence.
VERSION	AM845547
KEYWORDS	AM845547.1 GI:7941064
SOURCE	EST.
ORGANISM	human.

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Vertovski-Almeida, S., Briones, M. R.
1 (bases 1 to 100)
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 100)

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT	20202663
	Contact: Simpson A.J.G.

FEATURES
 source
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL.
<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=6t2-MR1-CIT0058-291199-003-d02a13-1999-11-29a1t4=1>
 Seq primer: puc 18 forward
 High quality sequence start: 30
 High quality sequence stop: 99.
 Location/Qualifiers
 1..100

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CR0058"
/dev_stage="Adult"
/notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No. 1967,16 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT
17 a 34 c 11 g 38 t

```

Query Match	Similarity	Score	DB	Length
Best Local	57.3%	Pred. No. 5.3e+04		100
Matches	47	Conservative	0	Mismatches 35; Indels 0; Gaps 0;
775	agaatataatcatctctaaacatacagcagcaaacctcttctgtgaagtgattcca	834		
82	aatgtgtaataaagcaaaacgctagccaggagagagacccagacaaaggaaggaaagctcta	23		
835	gtcgatgaattgaatgacacta	856		
22	cagggtacatagattgtgacta	1		

RESULT	12					
LOCUS	D45290/c					
DEFINITION	D45290	100 bp	mRNA	linear	EST	30-DEC-1995
ACCESSION	HUHHG3360	Human cerebral cortex				
VERSION	D45290.1					
KEYWORDS	EST.	GI:1136686				
SOURCE	human.					

REFERENCE	1 (bases 1 to 100)
AUTHORS	Takahashi, N., Hashida, H., Zhao, N., Misumi, Y. and Sakaki, Y.
TITLE	High-density cDNA filter analysis of the expression profiles of the
JOURNAL	genes preferentially expressed in human brain
MEDLINE	Gene 164, 219-227 (1995)
COMMENT	96069586
	Contact: Nobuaki Takahashi

COMMENT	FEATURES
Contact: Nobuaki Takahashi Institute of Medical Science University of Tokyo Shirokanedai 4-6-1, Minato-ku, Tokyo, Japan 108 Tel: 03-5449-5625 Fax: 03-5449-5445.	location/Qualifiers 1..100

BASE COUNT	ORIGIN	35 a	19 c	18 g	28 t
	/clone_11b="Human cerebral cortex"				
	/note="Adult male cerebral cortex tissue."				

Query Match	0.68;	Score 26;	DB 10;	Length 100;
Best Local Similarity	59.5%;	Pred. No. 5.3e+04;		
Matches 44;	Conservative	0;	Mismatches 30;	Indels 0;
				Gaps 0;
QY	853	actctactctgtaattcttgagctgacacctgagtttatatgctgctaactcaagtagagagag	912	
Db	79	ACCAAAACAGCTTTTATATAGTATGAGATTGTAAATTAAGTTTGAATAACGAGAAAGTGTCAGT	20	
QY	913	ccaccacacatttct	926	
Db	19	TCACCAACTTTGAT	6	

RESULT	13
AZ826437	
LOCUS	AZ826437
DEFINITION	71 bp DNA linear GSS 20-FEB-2001
ACCESSION	ZM0102K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
VERSION	AZ826437
KEYWORDS	AZ826437.1 GI:12996345
SOURCE	GSS.
ORGANISM	house mouse,
	house mouse,
	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Eukariyotica; Metazoa; Choriata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	Dunn,D., Aoyagi,A., Barber,M., Becarro,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606

Query Match 0.6%; Score 25.8; DB 12; Length 99;
Best Local Similarity 57.0%; Pred. No. 6e-04;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
OY 1905 caaggtatctatctagtggtgtgtatgtcagtgatgacagcggtggaactacaagtgtgt 1964
DB 16 CAATGGAACCCCTGGTCTTACGATCTGTCAANACAGAGGATTCTGGTACTACACATGCNC 75
OY 1965 ggccaacaccactctggac 1983
DB 76 TGCACCAACACTCTGGGC 94

Search completed: August 13, 2002, 21:18:23
Job time: 6465 sec